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June 3, 2002

PATENT APPLICATION
Attorney's Docket No.: 0399.1212-005

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	John Wyrick, Richard A. Young, Bing Ren, Francois Robert and Itamar Simon		
Application No.:	10/032,281	Group:	1651
Filed:	December 21, 2001	Examiner:	Not Assigned
For:	Genome-Wide Location and Function of DNA Binding Proteins		

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as First Class Mail in an envelope addressed to Assistant Commissioner for Patents, P.O. Box 2327, Arlington, VA 22202

on June 3, 2002 Stephanie L. Carta
Date Signature

Stephanie L. Carta
Typed or printed name of person signing certificate

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
P.O. Box 2327
Arlington, VA 22202

Sir:

In the Specification

Please replace the paragraph at page 7, lines 10 through 11 with the following paragraph:

Figures 7A-7C list the set of genes whose promoter regions are most likely to be bound by Ste112 by the analysis criteria described herein.

Please replace the paragraph at page 34, lines 8 through 28 with the following paragraph:

The genome-wide location of epitope-tagged Ste12p before and after pheromone treatment was investigated in three independent experiments. The set of genes whose promoter regions are most likely to be bound by Ste 12 by the analysis criteria (p-value < 0.005) described herein is listed in Figures 7A-7C; the upper panel shows genes whose expression is induced by alpha factor, whereas the lower panel shows genes whose expression is not significantly induced by alpha factor. Of the genes that are induced by alpha factor and are bound by Ste12, 11 are known to participate in various steps of the mating process (FIG2, AFR1, GIC2, STE12, KAR5, FUS1, AGA1, FUS3, CIK1, FAR1, FIG1) (Figure 8). FUS3 and STE12 encode components of the signal transduction pathway involved in the response to pheromone (Madhani *et al., Trends Genet., 14:*151 (1999)); AFR1 and GIC2 are required for the formation of mating projections (Konopka *et al., Mol. Cell Biol., 13:*6876 (1993); Brown *et al., Genes Dev., 11:*2972 (1997); Chen *et al., Genes Dev., 11:*2998 (1997)); FIG2, AGA1, FIG1 and FUS1 are involved in cell fusion (Erdman *et al., J. Cell Biol.,140:*461 (1999); Roy *et al., Mol. Cell Biol., 11:*4196 (1991); Truehart *et al., Mol. Cell biol., 7:*2316 (1987); McCaffrey *et al., Mol. Cell Biol., 7:*2680 (1987)); and CIK1 and KAR5 are required for nuclear fusion (Marsh, L. and Rose, M.D. in *The Moelcular and Cellular Biology of the Yeast Saccharomyces*, J.R. Pringle, J.R. Broach, E.W. Jones, Eds. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1997), vol. 3, pp. 827-888). Furthermore, FUS3 and FAR1 are required for pheromone-induced cell cycle arrest (Chang *et al., Cell, 63:*999 (1990); Fujimura, *Curr. Genet., 18:*395 (1990)).

Amendments to the specification are indicated in the attached "Marked Up Version of Amendments" (pages i - ii).

CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned at (978) 341-0036.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By 

Brian P. Turano
Registration No. 50,734
Telephone: (978) 341-0036
Facsimile: (978) 341-0136

Concord, MA 01742-9133
Dated:

June 7, 2002

MARKED UP VERSION OF AMENDMENTS

Specification Amendments Under 37 C.F.R. § 1.121(b)(1)(iii)

Replace the paragraph at page 7, lines 10 through 11 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figures 7A-7C list[s] the set of genes whose promoter regions are most likely to be bound by Ste112 by the analysis criteria described herein.

Replace the paragraph at page 34, lines 8 through 28 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

The genome-wide location of epitope-tagged Ste12p before and after pheromone treatment was investigated in three independent experiments. The set of genes whose promoter regions are most likely to be bound by Ste 12 by the analysis criteria (p-value < 0.005) described herein is listed in Figures 7A-7C; the upper panel shows genes whose expression is induced by alpha factor, whereas the lower panel shows genes whose expression is not significantly induced by alpha factor. Of the genes that are induced by alpha factor and are bound by Ste12, 11 are known to participate in various steps of the mating process (FIG2, AFR1, GIC2, STE12, KAR5, FUS1, AGA1, FUS3, CIK1, FAR1, FIG1) (Figure 8). FUS3 and STE12 encode components of the signal transduction pathway involved in the response to pheromone (Madhani *et al., Trends Genet., 14:*151 (1999)); AFR1 and GIC2 are required for the formation of mating projections (Konopka *et al., Mol. Cell Biol., 13:*6876 (1993); Brown *et al., Genes Dev., 11:*2972 (1997); Chen *et al., Genes Dev., 11:*2998 (1997)); FIG2, AGA1, FIG1 and FUS1 are involved in cell fusion (Erdman *et al., J. Cell Biol.,140:*461 (1999); Roy *et al., Mol. Cell Biol., 11:*4196 (1991); Truehart *et al., Mol. Cell biol., 7:*2316 (1987); McCaffrey *et al., Mol. Cell Biol., 7:*2680 (1987)); and CIK1 and KAR5 are required for nuclear fusion (Marsh, L. and Rose, M.D. in *The Moelcular and Cellular Biology of the Yeast Saccharomyces*, J.R. Pringle, J.R. Broach, E.W. Jones, Eds. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1997),

vol. 3, pp. 827-888). Furthermore, FUS3 and FAR1 are required for pheromone-induced cell cycle arrest (Chang *et al., Cell, 63:*999 (1990); Fujimura, *Curr. Genet., 18:*395 (1990)).